What is Claimed is:

1. A method for haplotyping the Fc fragment of IgE, high affinity I, receptor for; alpha polypeptide (FCER1A) gene of an individual, which comprises determining which of the FCER1A haplotypes shown in the table immediately below defines one copy of the individual's FCER1A gene, wherein the determining step comprises identifying the phased sequence of nucleotides present at each of PS1-PS22 on at least one copy of the individual's FCER1A gene, and wherein each of the FCER1A haplotypes comprises a sequence of polymorphisms whose positions and identities are set forth in the table immediately below:

PS Number(a)	PS Position (b)	Haplotype Number(c)									
		1	2	3	4	5	6	7	8	9	10
PS1	586	T	T	T	T	G	T	T	T	T	T
PS2	657	C	T	T	C	C	C	C	C	T	C
PS3	906	T	T	T	C	T	T	T	T	T	T
PS4	913	A	A	A	A	A	A	A	A	A	A
PS5	1077	C	C	C	C	C	C	C	C	C	C
PS6	1468	T	T	T	T	T	T	T	T	T	T
PS7	1474	C	C	C	C	C	C	C	C	C	C
PS8	1610	C	C	C	C	C	T	T	T	C	T
PS9	2422	A	A	A	A	A	A	A	A	G	A
PS10	2738	A	A	A	A	A	A	G	A	A	A
PS11	2789	G	G	G	G	G	G	G	G	G	A
PS12	2934	T	T	T	T	T	T	T	T	T	T
PS13	3000	G	G	G	G	G	G	G	G	G	A
PS14	3044	G	G	G	G	G	G	G	G	G	G
PS15	4552	G	G	G	G	G	A	A	G	G	G
PS16	4822	C	C	C	C	C	C	C	C	C	C
PS17	4999	T	C	C	T	T	T	T	T	C	T
PS18	5077	T	T	T	T	T	C	C	T	T	T
PS19	6535	C	C	C	C	C	C	C	C	C	C
PS20	6625	T	T	T	T	T	T	T	T	T	T
PS21	6650	A	A	A	A	A	A	G	A	A	A
PS22	6714	G	G	A	G	G	G	G	G	G	G

PS Number(a)	PS Position (b)	Haplotype Number(c)									
		11	12	13	14	15	16	17	18	19	20
PS1	586	G	T	T	T	T	T	T	T	T	T
PS2	657	C	C	C	T	C	C	C	C	T	T
PS3	906	T	T	T	T	T	T	T	T	T	T
PS4	913	A	A	A	A	A	A	A	T	A	A
PS5	1077	C	C	C	C	C	C	C	C	C	A
PS6	1468	C	T	T	T	T	T	T	T	T	T
PS7	1474	C	C	C	C	A	C	C	C	C	C
PS8	1610	C	C	T	T	T	C	T	T	C	T
PS9	2422	A	A	A	A	A	A	A	A	A	A
PS10	2738	A	A	A	A	A	A	G	A	A	A
PS11	2789	G	G	G	G	G	G	G	G	G	G
PS12	2934	C	T	T	T	T	T	T	T	T	T
PS13	3000	G	G	G	G	G	G	G	G	G	G
PS14	3044	G	G	G	G	G	A	G	G	G	G
PS15	4552	G	G	A	G	G	G	G	A	G	A
PS16	4822	C	C	C	C	C	C	C	C	T	C
PS17	4999	T	T	T	C	T	T	T	T	C	C
PS18	5077	T	T	C	T	T	T	T	C	T	C
PS19	6535	C	A	C	C	C	A	C	C	C	C
PS20	6625	C	T	T	T	T	T	T	T	T	T
PS21	6650	A	A	G	A	A	A	A	A	A	A
PS22	6714	G	G	G	A	G	G	G	G	A	G

(a) PS = polymorphic site;
(b) Position of PS within SEQ ID NO:1;
(c) Alleles for haplotypes are presented 5′ to 3′ in each column.

2. A method for haplotyping the Fc fragment of IgE, high affinity I, receptor for; alpha polypeptide (FCER1A) gene of an individual, which comprises determining which of the FCER1A haplotype pairs shown in the table immediately below defines both copies of the individual's FCER1A gene, wherein the determining step comprises identifying the phased sequence of nucleotides present at each of PS1-PS22 on both copies of the individual's FCER1A gene, and wherein each of the FCER1A haplotype pairs consists of first and second haplotypes which comprise first and second sequences of polymorphisms whose positions and identities are set forth in the table immediately below:

PS Number(a)	PS Position(b)	Haplotype Pair(c) Part 1														
		1/1	1/2	1/3	1/4	1/5	1/7	1/11	1/12	1/15	1/16	1/17	1/20	2/2	2/3	2/4
PS1	586	T	T	T	T	T/G	T	T/G	T	T	T	T	T	T	T	T
PS2	657	C	C/T	C/T	C	C	C	C	C	C	C	C	C/T	T	T	C/T
PS3	906	T	T	T	T/C	T	T	T	T	T	T	T	T	T	T	T/C
PS4	913	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A
PS5	1077	C	C	C	C	C	C	C	C	C	C	C	C/A	C	C	C
PS6	1468	T	T	T	T	T	T	T/C	T	T	T	T	T	T	T	T
PS7	1474	C	C	C	C	C	C	C	C	C/A	C	C	C	C	C	C
PS8	1610	C	C	C	C	C	C/T	C	C	C/T	C	C/T	C/T	C	C	C
PS9	2422	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A
PS10	2738	A	A	A	A	A	A/G	A	A	A	A	A/G	A	A	A	A
PS11	2789	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G
PS12	2934	T	T	T	T	T	T	T/C	T	T	T	T	T	T	T	T
PS13	3000	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G
PS14	3044	G	G	G	G	G	G	G	G	G	G/A	G	G	G	G	G
PS15	4552	G	G	G	G	G	G/A	G	G	G	G	G	G/A	G	G	G
PS16	4822	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C
PS17	4999	T	T/C	T/C	T	T	T	T	T	T	T	T	T/C	C	C	T/C
PS18	5077	T	T	T	T	T	T/C	T	T	T	T	T/C	T/C	T	T	T
PS19	6535	C	C	C	C	C	C	C	C/A	C	C/A	C	C	C	C	C
PS20	6625	T	T	T	T	T	T	T/C	T	T	T	T	T	T	T	T
PS21	6650	A	A	A	A	A	A/G	A	A	A	A	A	A	A	A	A
PS22	6714	G	G	G/A	G	G	G	G	G	G	G	G	G	G	G/A	G

PS Number(a)	PS Position(b)	Haplotype Pair(c) Part 2														
		2/6	2/9	2/10	2/13	2/14	3/3	3/4	3/5	3/6	3/9	3/12	3/15	3/19	4/4	4/5
PS1	586	T	T	T	T	T	T	T	T/G	T	T	T	T	T	T	T/G
PS2	657	C/T	T	C/T	C/T	T	T	C/T	C/T	C/T	T	C/T	C/T	T	C	C
PS3	906	T	T	T	T	T	T	T/C	T	T	T	T	T	T	C	T/C
PS4	913	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A
PS5	1077	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C
PS6	1468	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T
PS7	1474	C	C	C	C	C	C	C	C	C	C	C	C/A	C	C	C
PS8	1610	C/T	C	C/T	C/T	C/T	C	C	C	C/T	C	C	C/T	C	C	C
PS9	2422	A	A/G	A	A	A	A	A	A	A	A/G	A	A	A	A	A
PS10	2738	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A
PS11	2789	G	G	G/A	G	G	G	G	G	G	G	G	G	G	G	G
PS12	2934	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T
PS13	3000	G	G	G/A	G	G	G	G	G	G	G	G	G	G	G	G
PS14	3044	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G
PS15	4552	G/A	G	G	G/A	G	G	G	G	G/A	G	G	G	G	G	G
PS16	4822	C	C	C	C	C	C	C	C	C	C	C	C	C/T	C	C
PS17	4999	T/C	C	T/C	T/C	T/C	C	T/C	T/C	T/C	C	T/C	T/C	C	T	T
PS18	5077	T/C	T	T	T/C	T	T	T	T	T/C	T	T	T	T	T	T
PS19	6535	C	C	C	C	C	C	C	C	C	C	C/A	C	C	C	C
PS20	6625	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T
PS21	6650	A	A	A	A/G	A	A	A	A	A	A	A	A	A	A	A
PS22	6714	G	G	G	G	G/A	A	G/A	G/A	G/A	G/A	G/A	G/A	A	G	G

PS Number(a)	PS Position(b)	Haplotype Pair(c) Part 3													
		4/6	4/8	4/11	4/13	5/5	5/11	5/15	6/6	6/7	6/8	6/10	6/18	7/7	7/10
PS1	586	T	T	T/G	T	G	G	T/G	T	T	T	T	T	T	T
PS2	657	C	C	C	C	C	C	C	C	C	C	C	C	C	C
PS3	906	T/C	T/C	T/C	T/C	T	T	T	T	T	T	T	T	T	T
PS4	913	A	A	A	A	A	A	A	A	A	A	A	A/T	A	A
PS5	1077	C	C	C	C	C	C	C	C	C	C	C	C	C	C
PS6	1468	T	T	T/C	T	T	T/C	T	T	T	T	T	T	T	T
PS7	1474	C	C	C	C	C	C	C/A	C	C	C	C	C	C	C
PS8	1610	C/T	C/T	C	C/T	C	C	C/T	T	T	T	T	T	T	T
PS9	2422	A	A	A	A	A	A	A	A	A	A	A	A	A	A
PS10	2738	A	A	A	A	A	A	A	A	A/G	A	A	A	G	A/G
PS11	2789	G	G	G	G	G	G	G	G	G	G	G/A	G	G	G/A
PS12	2934	T	T	T/C	T	T	T/C	T	T	T	T	T	T	T	T
PS13	3000	G	G	G	G	G	G	G	G	G	G	G/A	G	G	G/A
PS14	3044	G	G	G	G	G	G	G	G	G	G	G	G	G	G
PS15	4552	G/A	G	G	G/A	G	G	G	A	A	G/A	G/A	A	A	G/A
PS16	4822	C	C	C	C	C	C	C	C	C	C	C	C	C	C
PS17	4999	T	T	T	T	T	T	T	T	T	T	T	T	T	T
PS18	5077	T/C	T	T	T/C	T	T	T	C	C	T/C	T/C	C	C	T/C
PS19	6535	C	C	C	C	C	C	C	C	C	C	C	C	C	C
PS20	6625	T	T	T/C	T	T	T/C	T	T	T	T	T	T	T	T
PS21	6650	A	A	A	A/G	A	A	A	A	A/G	A	A	A	G	A/G
PS22	6714	G	G	G	G	G	G	G	G	G	G	G	G	G	G

(a) PS = polymorphic site;
(b) Position of PS in SEQ ID NO:1;
(c) Haplotype pairs are represented as 1st haplotype/2nd haplotype; with alleles of each haplotype shown 5′ to 3′ as 1st polymorphism/2nd polymorphism in each column.

3. A method for genotyping the Fc fragment of IgE, high affinity I, receptor for; alpha polypeptide (FCER1A) gene of an individual, comprising determining for the two copies of the FCER1A gene present in the individual the identity of the nucleotide pair at one or more polymorphic sites (PS) selected from the group consisting of PS1, PS2, PS3, PS4, PS5, PS6, PS7, PS8, PS9, PS10, PS11, PS12, PS13, PS14, PS15, PS16, PS17, PS18, PS19, PS20, PS21 and PS22, wherein the one or more polymorphic sites (PS) have the position and alternative alleles shown in SEQ ID NO:1.

4. The method of claim 3, wherein the determining step comprises:

(a) isolating from the individual a nucleic acid mixture comprising both copies of the FCER1A gene, or a fragment thereof, that are present in the individual;

(b) amplifying from the nucleic acid mixture a target region containing one of the selected polymorphic sites;

(c) hybridizing a primer extension oligonucleotide to one allele of the amplified target region, wherein the oligonucleotide is designed for genotyping the selected polymorphic site in the target region;

(d) performing a nucleic acid template-dependent, primer extension reaction on the

hybridized oligonucleotide in the presence of at least one terminator of the reaction, wherein the terminator is complementary to one of the alternative nucleotides present at the selected polymorphic site; and

(e) detecting the presence and identity of the terminator in the extended oligonucleotide.

5. The method of claim 3, which comprises determining for the two copies of the FCER1A gene present in the individual the identity of the nucleotide pair at each of PS1-PS22.

6. A method for haplotyping the Fc fragment of IgE, high affinity I, receptor for; alpha polypeptide (FCER1A) gene of an individual which comprises determining, for one copy of the FCER1A gene present in the individual, the identity of the nucleotide at two or more polymorphic sites (PS) selected from the group consisting of PS1, PS2, PS3, PS4, PS5, PS6, PS7, PS8, PS9, PS10, PS11, PS12, PS13, PS14, PS15, PS16, PS17, PS18, PS19, PS20, PS21 and PS22, wherein the selected PS have the position and alternative alleles shown in SEQ ID NO:1.

7. The method of claim 6, wherein the determining step comprises:

(a) isolating from the individual a nucleic acid sample containing only one of the two copies of the FCER1A gene, or a fragment thereof, that is present in the individual;

(b) amplifying from the nucleic acid sample a target region containing one of the selected polymorphic sites;

(c) hybridizing a primer extension oligonucleotide to one allele of the amplified target region, wherein the oligonucleotide is designed for haplotyping the selected polymorphic site in the target region;

(d) performing a nucleic acid template-dependent, primer extension reaction on the hybridized oligonucleotide in the presence of at least one terminator of the reaction, wherein the terminator is complementary to one of the alternative nucleotides present at the selected polymorphic site; and

(e) detecting the presence and identity of the terminator in the extended oligonucleotide.

8. A method for predicting a haplotype pair for the Fc fragment of IgE, high affinity I, receptor for; alpha polypeptide (FCER1A) gene of an individual comprising:

(a) identifying a FCER1A genotype for the individual, wherein the genotype comprises the nucleotide pair at two or more polymorphic sites (PS) selected from the group consisting of PS1, PS2, PS3, PS4, PS5, PS6, PS7, PS8, PS9, PS10, PS11, PS12, PS13, PS14, PS15, PS16, PS17, PS18, PS19, PS20, PS21 and PS22, wherein the selected PS have the position and alternative alleles shown in SEQ ID NO:1;

(b) comparing the genotype to the haplotype pair data set forth in the table immediately below; and

(c) determining which haplotype pair is consistent with the genotype of the individual and with the haplotype pair data

PS Number(a)	PS Position(b)	Haplotype Pair(c) Part 1														
		1/1	1/2	1/3	1/4	1/5	1/7	1/11	1/12	1/15	1/16	1/17	1/20	2/2	2/3	2/4
PS1	586	T	T	T	T	T/G	T	T/G	T	T	T	T	T	T	T	T
PS2	657	C	C/T	C/T	C	C	C	C	C	C	C	C	C/T	T	T	C/T
PS3	906	T	T	T	T/C	T	T	T	T	T	T	T	T	T	T	T/C
PS4	913	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A
PS5	1077	C	C	C	C	C	C	C	C	C	C	C	C/A	C	C	C
PS6	1468	T	T	T	T	T	T	T/C	T	T	T	T	T	T	T	T
PS7	1474	C	C	C	C	C	C	C	C	C/A	C	C	C	C	C	C
PS8	1610	C	C	C	C	C	C/T	C	C	C/T	C	C/T	C/T	C	C	C
PS9	2422	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A
PS10	2738	A	A	A	A	A	A/G	A	A	A	A	A/G	A	A	A	A
PS11	2789	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G
PS12	2934	T	T	T	T	T	T	T/C	T	T	T	T	T	T	T	T
PS13	3000	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G
PS14	3044	G	G	G	G	G	G	G	G	G	G/A	G	G	G	G	G
PS15	4552	G	G	G	G	G	G/A	G	G	G	G	G	G/A	G	G	G
PS16	4822	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C
PS17	4999	T	T/C	T/C	T	T	T	T	T	T	T	T	T/C	C	C	T/C
PS18	5077	T	T	T	T	T	T/C	T	T	T	T	T/C	T/C	T	T	T
PS19	6535	C	C	C	C	C	C	C	C/A	C	C/A	C	C	C	C	C
PS20	6625	T	T	T	T	T	T	T/C	T	T	T	T	T	T	T	T
PS21	6650	A	A	A	A	A	A/G	A	A	A	A	A	A	A	A	A
PS22	6714	G	G	G/A	G	G	G	G	G	G	G	G	G	G	G/A	G

PS Number(a)	PS Position(b)	Haplotype Pair(c) Part 2														
		2/6	2/9	2/10	2/13	2/14	3/3	3/4	3/5	3/6	3/9	3/12	3/15	3/19	4/4	4/5
PS1	586	T	T	T	T	T	T	T	T/G	T	T	T	T	T	T	T/G
PS2	657	C/T	T	C/T	C/T	T	T	C/T	C/T	C/T	T	C/T	C/T	T	C	C
PS3	906	T	T	T	T	T	T	T/C	T	T	T	T	T	T	C	T/C
PS4	913	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A
PS5	1077	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C
PS6	1468	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T
PS7	1474	C	C	C	C	C	C	C	C	C	C	C	C/A	C	C	C
PS8	1610	C/T	C	C/T	C/T	C/T	C	C	C	C/T	C	C	C/T	C	C	C
PS9	2422	A	A/G	A	A	A	A	A	A	A	A/G	A	A	A	A	A
PS10	2738	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A
PS11	2789	G	G	G/A	G	G	G	G	G	G	G	G	G	G	G	G
PS12	2934	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T
PS13	3000	G	G	G/A	G	G	G	G	G	G	G	G	G	G	G	G
PS14	3044	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G
PS15	4552	G/A	G	G	G/A	G	G	G	G	G/A	G	G	G	G	G	G
PS16	4822	C	C	C	C	C	C	C	C	C	C	C	C	C/T	C	C
PS17	4999	T/C	C	T/C	T/C	T/C	C	T/C	T/C	T/C	C	T/C	T/C	C	T	T
PS18	5077	T/C	T	T	T/C	T	T	T	T	T/C	T	T	T	T	T	T
PS19	6535	C	C	C	C	C	C	C	C	C	C	C/A	C	C	C	C
PS20	6625	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T
PS21	6650	A	A	A	A/G	A	A	A	A	A	A	A	A	A	A	A
PS22	6714	G	G	G	G	G/A	A	G/A	G/A	G/A	G/A	G/A	G/A	A	G	G

PS Number(a)	PS Position(b)	Haplotype Pair(c) Part 3													
		4/6	4/8	4/11	4/13	5/5	5/11	5/15	6/6	6/7	6/8	6/10	6/18	7/7	7/10
PS1	586	T	T	T/G	T	G	G	T/G	T	T	T	T	T	T	T
PS2	657	C	C	C	C	C	C	C	C	C	C	C	C	C	C
PS3	906	T/C	T/C	T/C	T/C	T	T	T	T	T	T	T	T	T	T
PS4	913	A	A	A	A	A	A	A	A	A	A	A	A/T	A	A
PS5	1077	C	C	C	C	C	C	C	C	C	C	C	C	C	C
PS6	1468	T	T	T/C	T	T	T/C	T	T	T	T	T	T	T	T
PS7	1474	C	C	C	C	C	C	C/A	C	C	C	C	C	C	C
PS8	1610	C/T	C/T	C	C/T	C	C	C/T	T	T	T	T	T	T	T
PS9	2422	A	A	A	A	A	A	A	A	A	A	A	A	A	A
PS10	2738	A	A	A	A	A	A	A	A	A/G	A	A	A	G	A/G
PS11	2789	G	G	G	G	G	G	G	G	G	G	G/A	G	G	G/A
PS12	2934	T	T	T/C	T	T	T/C	T	T	T	T	T	T	T	T
PS13	3000	G	G	G	G	G	G	G	G	G	G	G/A	G	G	G/A
PS14	3044	G	G	G	G	G	G	G	G	G	G	G	G	G	G
PS15	4552	G/A	G	G	G/A	G	G	G	A	A	G/A	G/A	A	A	G/A
PS16	4822	C	C	C	C	C	C	C	C	C	C	C	C	C	C
PS17	4999	T	T	T	T	T	T	T	T	T	T	T	T	T	T
PS18	5077	T/C	T	T	T/C	T	T	T	C	C	T/C	T/C	C	C	T/C
PS19	6535	C	C	C	C	C	C	C	C	C	C	C	C	C	C
PS20	6625	T	T	T/C	T	T	T/C	T	T	T	T	T	T	T	T
PS21	6650	A	A	A	A/G	A	A	A	A	A/G	A	A	A	G	A/G
PS22	6714	G	G	G	G	G	G	G	G	G	G	G	G	G	G

(a) PS = polymorphic site;
(b) Position of PS in SEQ ID NO:1;
(c) Haplotype pairs are represented as 1st haplotype/2nd haplotype; with alleles of each haplotype shown 5′ to 3′ as 1st polymorphism/2nd polymorphism in each column.

9. The method of claim 8, wherein the identified genotype of the individual comprises the nucleotide pair at each of PS1-PS22, which have the position and alternative alleles shown in SEQ ID NO:1.

10. A method for identifying an association between a trait and at least one haplotype or haplotype pair of the Fc fragment of IgE, high affinity I, receptor for; alpha polypeptide (FCER1A) gene which comprises comparing the frequency of the haplotype or haplotype pair in a population exhibiting the trait with the frequency of the haplotype or haplotype pair in a reference population, wherein the haplotype is selected from haplotypes 1-20 shown in the table presented immediately below, wherein each of the haplotypes comprises a sequence of polymorphisms whose positions and identities are set forth in the table immediately below:

PS Number(a)	PS Position (b)	Haplotype Number(c)									
		1	2	3	4	5	6	7	8	9	10
PS1	586	T	T	T	T	G	T	T	T	T	T
PS2	657	C	T	T	C	C	C	C	C	T	C
PS3	906	T	T	T	C	T	T	T	T	T	T
PS4	913	A	A	A	A	A	A	A	A	A	A
PS5	1077	C	C	C	C	C	C	C	C	C	C
PS6	1468	T	T	T	T	T	T	T	T	T	T
PS7	1474	C	C	C	C	C	C	C	C	C	C
PS8	1610	C	C	C	C	C	T	T	T	C	T
PS9	2422	A	A	A	A	A	A	A	A	G	A
PS10	2738	A	A	A	A	A	A	G	A	A	A
PS11	2789	G	G	G	G	G	G	G	G	G	A
PS12	2934	T	T	T	T	T	T	T	T	T	T
PS13	3000	G	G	G	G	G	G	G	G	G	A
PS14	3044	G	G	G	G	G	G	G	G	G	G
PS15	4552	G	G	G	G	G	A	A	G	G	G
PS16	4822	C	C	C	C	C	C	C	C	C	C
PS17	4999	T	C	C	T	T	T	T	T	C	T
PS18	5077	T	T	T	T	T	C	C	T	T	T
PS19	6535	C	C	C	C	C	C	C	C	C	C
PS20	6625	T	T	T	T	T	T	T	T	T	T
PS21	6650	A	A	A	A	A	A	G	A	A	A
PS22	6714	G	G	A	G	G	G	G	G	G	G

PS Number(a)	PS Position (b)	Haplotype Number(c)									
		11	12	13	14	15	16	17	18	19	20
PS1	586	G	T	T	T	T	T	T	T	T	T
PS2	657	C	C	C	T	C	C	C	C	T	T
PS3	906	T	T	T	T	T	T	T	T	T	T
PS4	913	A	A	A	A	A	A	A	T	A	A
PS5	1077	C	C	C	C	C	C	C	C	C	A
PS6	1468	C	T	T	T	T	T	T	T	T	T
PS7	1474	C	C	C	C	A	C	C	C	C	C
PS8	1610	C	C	T	T	T	C	T	T	C	T
PS9	2422	A	A	A	A	A	A	A	A	A	A
PS10	2738	A	A	A	A	A	A	G	A	A	A
PS11	2789	G	G	G	G	G	G	G	G	G	G
PS12	2934	C	T	T	T	T	T	T	T	T	T
PS13	3000	G	G	G	G	G	G	G	G	G	G
PS14	3044	G	G	G	G	G	A	G	G	G	G
PS15	4552	G	G	A	G	G	G	G	A	G	A
PS16	4822	C	C	C	C	C	C	C	C	T	C
PS17	4999	T	T	T	C	T	T	T	T	C	C
PS18	5077	T	T	C	T	T	T	T	C	T	C
PS19	6535	C	A	C	C	C	A	C	C	C	C
PS20	6625	C	T	T	T	T	T	T	T	T	T
PS21	6650	A	A	G	A	A	A	A	A	A	A
PS22	6714	G	G	G	A	G	G	G	G	A	G

(a) PS = polymorphic site;
(b) Position of PS within SEQ ID NO:1;
(c) Alleles for haplotypes are presented 5′ to 3′ in each column;

and wherein the haplotype pair is selected from the haplotype pairs shown in the table immediately below, wherein each of the FCER1A haplotype pairs consists of first and second haplotypes which comprise first and second sequences of polymorphisms whose positions in SEQ ID NO:1 and identities are set forth in the table immediately below:

PS	PS	Haplotype Pair(c) Part 1														
Number(a)	Position(b)	1/1	1/2	1/3	1/4	1/5	1/7	1/11	1/12	1/15	1/16	1/17	1/20	2/2	2/3	2/4
PS1	586	T	T	T	T	T/G	T	T/G	T	T	T	T	T	T	T	T
PS2	657	C	C/T	C/T	C	C	C	C	C	C	C	C	C/T	T	T	C/T
PS3	906	T	T	T	T/C	T	T	T	T	T	T	T	T	T	T	T/C
PS4	913	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A
PS5	1077	C	C	C	C	C	C	C	C	C	C	C	C/A	C	C	C
PS6	1468	T	T	T	T	T	T	T/C	T	T	T	T	T	T	T	T
PS7	1474	C	C	C	C	C	C	C	C	C/A	C	C	C	C	C	C
PS8	1610	C	C	C	C	C	C/T	C	C	C/T	C	C/T	C/T	C	C	C
PS9	2422	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A
PS10	2738	A	A	A	A	A	A/G	A	A	A	A	A/G	A	A	A	A
PS11	2789	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G
PS12	2934	T	T	T	T	T	T	T/C	T	T	T	T	T	T	T	T
PS13	3000	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G
PS14	3044	G	G	G	G	G	G	G	G	G	G/A	G	G	G	G	G
PS15	4552	G	G	G	G	G	G/A	G	G	G	G	G	G/A	G	G	G
PS16	4822	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C
PS17	4999	T	T/C	T/C	T	T	T	T	T	T	T	T	T/C	C	C	T/C
PS18	5077	T	T	T	T	T	T/C	T	T	T	T	T/C	T/C	T	T	T
PS19	6535	C	C	C	C	C	C	C	C/A	C	C/A	C	C	C	C	C
PS20	6625	T	T	T	T	T	T	T/C	T	T	T	T	T	T	T	T
PS21	6650	A	A	A	A	A	A/G	A	A	A	A	A	A	A	A	A
PS22	6714	G	G	G/A	G	G	G	G	G	G	G	G	G	G	G/A	G

PS	PS	Haplotype Pair(c) Part 2														
Number(a)	Position(b)	2/6	2/9	2/10	2/13	2/14	3/3	3/4	3/5	3/6	3/9	3/12	3/15	3/19	4/4	4/5
PS1	586	T	T	T	T	T	T	T	T/G	T	T	T	T	T	T	T/G
PS2	657	C/T	T	C/T	C/T	T	T	C/T	C/T	C/T	T	C/T	C/T	T	C	C
PS3	906	T	T	T	T	T	T	T/C	T	T	T	T	T	T	C	T/C
PS4	913	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A
PS5	1077	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C
PS6	1468	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T
PS7	1474	C	C	C	C	C	C	C	C	C	C	C	C/A	C	C	C
PS8	1610	C/T	C	C/T	C/T	C/T	C	C	C	C/T	C	C	C/T	C	C	C
PS9	2422	A	A/G	A	A	A	A	A	A	A	A/G	A	A	A	A	A
PS10	2738	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A
PS11	2789	G	G	G/A	G	G	G	G	G	G	G	G	G	G	G	G
PS12	2934	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T
PS13	3000	G	G	G/A	G	G	G	G	G	G	G	G	G	G	G	G
PS14	3044	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G
PS15	4552	G/A	G	G	G/A	G	G	G	G	G/A	G	G	G	G	G	G
PS16	4822	C	C	C	C	C	C	C	C	C	C	C	C	C/T	C	C
PS17	4999	T/C	C	T/C	T/C	T/C	C	T/C	T/C	T/C	C	T/C	T/C	C	T	T
PS18	5077	T/C	T	T	T/C	T	T	T	T	T/C	T	T	T	T	T	T
PS19	6535	C	C	C	C	C	C	C	C	C	C	C/A	C	C	C	C
PS20	6625	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T
PS21	6650	A	A	A	A/G	A	A	A	A	A	A	A	A	A	A	A
PS22	6714	G	G	G	G	G/A	A	G/A	G/A	G/A	G/A	G/A	G/A	A	G	G

PS Number(a)	PS Position(b)	Haplotype Pair(c) Part 3													
		4/6	4/8	4/11	4/13	5/5	5/11	5/15	6/6	6/7	6/8	6/10	6/18	7/7	7/10
PS1	586	T	T	T/G	T	G	G	T/G	T	T	T	T	T	T	T
PS2	657	C	C	C	C	C	C	C	C	C	C	C	C	C	C
PS3	906	T/C	T/C	T/C	T/C	T	T	T	T	T	T	T	T	T	T
PS4	913	A	A	A	A	A	A	A	A	A	A	A	A/T	A	A
PS5	1077	C	C	C	C	C	C	C	C	C	C	C	C	C	C
PS6	1468	T	T	T/C	T	T	T/C	T	T	T	T	T	T	T	T
PS7	1474	C	C	C	C	C	C	C/A	C	C	C	C	C	C	C
PS8	1610	C/T	C/T	C	C/T	C	C	C/T	T	T	T	T	T	T	T
PS9	2422	A	A	A	A	A	A	A	A	A	A	A	A	A	A
PS10	2738	A	A	A	A	A	A	A	A	A/G	A	A	A	G	A/G
PS11	2789	G	G	G	G	G	G	G	G	G	G	G/A	G	G	G/A
PS12	2934	T	T	T/C	T	T	T/C	T	T	T	T	T	T	T	T
PS13	3000	G	G	G	G	G	G	G	G	G	G	G/A	G	G	G/A
PS14	3044	G	G	G	G	G	G	G	G	G	G	G	G	G	G
PS15	4552	G/A	G	G	G/A	G	G	G	A	A	G/A	G/A	A	A	G/A
PS16	4822	C	C	C	C	C	C	C	C	C	C	C	C	C	C
PS17	4999	T	T	T	T	T	T	T	T	T	T	T	T	T	T
PS18	5077	T/C	T	T	T/C	T	T	T	C	C	T/C	T/C	C	C	T/C
PS19	6535	C	C	C	C	C	C	C	C	C	C	C	C	C	C
PS20	6625	T	T	T/C	T	T	T/C	T	T	T	T	T	T	T	T
PS21	6650	A	A	A	A/G	A	A	A	A	A/G	A	A	A	G	A/G
PS22	6714	G	G	G	G	G	G	G	G	G	G	G	G	G	G

(a) PS = polymorphic site;
(b) Position of PS in SEQ ID NO:1;
(c) Haplotype pairs are represented as 1st haplotype/2nd haplotype; with alleles of each haplotype shown 5′ to 3′ as 1st polymorphism/2nd polymorphism in each column;

wherein a higher frequency of the haplotype or haplotype pair in the trait population than in the reference population indicates the trait is associated with the haplotype or haplotype pair.

11. The method of claim 10, wherein the trait is a clinical response to a drug targeting FCER1A or to a drug for treating a condition or disease predicted to be associated with FCER1A activity.

12. An isolated oligonucleotide designed for detecting a polymorphism in the Fc fragment of IgE, high affinity I, receptor for; alpha polypeptide (FCER1A) gene at a polymorphic site (PS) selected from the group consisting of PS1, PS2, PS3, PS4, PS5, PS6, PS7, PS8, PS9, PS10, PS11, PS12, PS13, PS14, PS15, PS16, PS17, PS18, PS19, PS20, PS21 and PS22, wherein the selected PS have the position and alternative alleles shown in SEQ ID NO:1.

13. The isolated oligonucleotide of claim 12, which is an allele-specific oligonucleotide that specifically hybridizes to an allele of the FCER1A gene at a region containing the polymorphic site.

14. The allele-specific oligonucleotide of claim 13, which comprises a nucleotide sequence selected from the group consisting of SEQ ID NOS:4-25, the complements of SEQ ID NOS:4-25, and SEQ ID NOS:26-69.

15. The isolated oligonucleotide of claim 12, which is a primer-extension oligonucleotide.

16. The primer-extension oligonucleotide of claim 15, which comprises a nucleotide sequence selected from the group consisting of SEQ ID NOS:70-113.

17. A kit for haplotyping or genotyping the Fc fragment of IgE, high affinity I, receptor for; alpha polypeptide (FCER1A) gene of an individual, which comprises a set of oligonucleotides designed to haplotype or genotype each of polymorphic sites (PS) PS1, PS2, PS3, PS4, PS5, PS6, PS7, PS8, PS9, PS10, PS11, PS12, PS13, PS14, PS15, PS16, PS17, PS18, PS19, PS20, PS21 and PS22, wherein the selected PS have the position and alternative alleles shown in SEQ ID NO:1.

18. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

(a) a first nucleotide sequence which comprises a Fc fragment of IgE, high affinity I, receptor for; alpha polypeptide (FCER1A) isogene, wherein the FCER1A isogene is selected from the group consisting of isogenes 1 and 3-20 shown in the table immediately below and wherein each of the isogenes comprises the regions of SEQ ID NO:1 shown in the table immediately below and wherein each of the isogenes 1 and 3-20 is further defined by the corresponding sequence of polymorphisms whose positions and identities are set forth in the table immediately below; and

Regions Examined(a)	PS Number(b)	PS Position (c)	Isogene Number(d) (Part 1)								
			1	3	4	5	6	7	8	9	10
319-1709	PS1	586	T	T	T	G	T	T	T	T	T
319-1709	PS2	657	C	T	C	C	C	C	C	T	C
319-1709	PS3	906	T	T	C	T	T	T	T	T	T
319-1709	PS4	913	A	A	A	A	A	A	A	A	A
319-1709	PS5	1077	C	C	C	C	C	C	C	C	C
319-1709	PS6	1468	T	T	T	T	T	T	T	T	T
319-1709	PS7	1474	C	C	C	C	C	C	C	C	C
319-1709	PS8	1610	C	C	C	C	T	T	T	C	T
2351-3067	PS9	2422	A	A	A	A	A	A	A	G	A
2351-3067	PS10	2738	A	A	A	A	A	G	A	A	A
2351-3067	PS11	2789	G	G	G	G	G	G	G	G	A
2351-3067	PS12	2934	T	T	T	T	T	T	T	T	T
2351-3067	PS13	3000	G	G	G	G	G	G	G	G	A
2351-3067	PS14	3044	G	G	G	G	G	G	G	G	G
4359-5177	PS15	4552	G	G	G	G	A	A	G	G	G
4359-5177	PS16	4822	C	C	C	C	C	C	C	C	C
4359-5177	PS17	4999	T	C	T	T	T	T	T	C	T
4359-5177	PS18	5077	T	T	T	T	C	C	T	T	T
6200-7073	PS19	6535	C	C	C	C	C	C	C	C	C
6200-7073	PS20	6625	T	T	T	T	T	T	T	T	T
6200-7073	PS21	6650	A	A	A	A	A	G	A	A	A
6200-7073	PS22	6714	G	A	G	G	G	G	G	G	G

Regions Examined(a)	PS Number(b)	PS Position (c)	Isogene Number(d) (Part 2)									
			11	12	13	14	15	16	17	18	19	20
319-1709	PS1	586	G	T	T	T	T	T	T	T	T	T
319-1709	PS2	657	C	C	C	T	C	C	C	C	T	T
319-1709	PS3	906	T	T	T	T	T	T	T	T	T	T
319-1709	PS4	913	A	A	A	A	A	A	A	T	A	A
319-1709	PS5	1077	C	C	C	C	C	C	C	C	C	A
319-1709	PS6	1468	C	T	T	T	T	T	T	T	T	T
319-1709	PS7	1474	C	C	C	C	A	C	C	C	C	C
319-1709	PS8	1610	C	C	T	T	T	C	T	T	C	T
2351-3067	PS9	2422	A	A	A	A	A	A	A	A	A	A
2351-3067	PS10	2738	A	A	A	A	A	A	G	A	A	A
2351-3067	PS11	2789	G	G	G	G	G	G	G	G	G	G
2351-3067	PS12	2934	C	T	T	T	T	T	T	T	T	T
2351-3067	PS13	3000	G	G	G	G	G	G	G	G	G	G
2351-3067	PS14	3044	G	G	G	G	G	A	G	G	G	G
4359-5177	PS15	4552	G	G	A	G	G	G	G	A	G	A
4359-5177	PS16	4822	C	C	C	C	C	C	C	C	T	C
4359-5177	PS17	4999	T	T	T	C	T	T	T	T	C	C
4359-5177	PS18	5077	T	T	C	T	T	T	T	C	T	C
6200-7073	PS19	6535	C	A	C	C	C	A	C	C	C	C
6200-7073	PS20	6625	C	T	T	T	T	T	T	T	T	T
6200-7073	PS21	6650	A	A	G	A	A	A	A	A	A	A
6200-7073	PS22	6714	G	G	G	A	G	G	G	G	A	G

(a) Region examined represents the nucleotide positions defining the start and stop positions within the 1st SEQ ID NO of the sequenced region;
(b) PS = polymorphic site;
(c) Position of PS in SEQ ID NO:1;
(d) Alleles for isogenes are presented 5′ to 3′ in each column;

(b) a second nucleotide sequence which is complementary to the first nucleotide sequence.

19. The isolated polynucleotide of claim 18, which is a DNA molecule and comprises both the first and second nucleotide sequences and further comprises expression regulatory elements operably linked to the first nucleotide sequence.

20. A recombinant nonhuman organism transformed or transfected with the isolated polynucleotide of claim 19, wherein the organism expresses a FCER1A protein that is encoded by the first nucleotide sequence.

21. The recombinant nonhuman organism of claim 20, which is a transgenic animal.

22. An isolated fragment of a Fc fragment of IgE, high affinity I, receptor for; alpha polypeptide (FCER1A) isogene, wherein the fragment comprises at least 10 nucleotides in one of the regions of SEQ ID NO:1 shown in the table immediately below and wherein the fragment

comprises one or more polymorphisms selected from the group consisting of guanine at PS1, cytosine at PS2, cytosine at PS3, thymine at PS4, adenine at PS5, cytosine at PS6, adenine at PS7, thymine at PS8, guanine at PS9, guanine at PS10, adenine at PS11, cytosine at PS12, adenine at PS13, adenine at PS14, adenine at PS15, thymine at PS16, thymine at PS17, cytosine at PS18, adenine at PS19, cytosine at PS20, guanine at PS21 and adenine at PS22, wherein the selected polymorphism has the position set forth in the table immediately below:

Regions Examined(a)	PS Number(b)	PS Position (c)	Isogene Number(d) (Part 1)								
			1	3	4	5	6	7	8	9	10
319-1709	PS1	586	T	T	T	G	T	T	T	T	T
319-1709	PS2	657	C	T	C	C	C	C	C	T	C
319-1709	PS3	906	T	T	C	T	T	T	T	T	T
319-1709	PS4	913	A	A	A	A	A	A	A	A	A
319-1709	PS5	1077	C	C	C	C	C	C	C	C	C
319-1709	PS6	1468	T	T	T	T	T	T	T	T	T
319-1709	PS7	1474	C	C	C	C	C	C	C	C	C
319-1709	PS8	1610	C	C	C	C	T	T	T	C	T
2351-3067	PS9	2422	A	A	A	A	A	A	A	G	A
2351-3067	PS10	2738	A	A	A	A	A	G	A	A	A
2351-3067	PS11	2789	G	G	G	G	G	G	G	G	A
2351-3067	PS12	2934	T	T	T	T	T	T	T	T	T
2351-3067	PS13	3000	G	G	G	G	G	G	G	G	A
2351-3067	PS14	3044	G	G	G	G	G	G	G	G	G
4359-5177	PS15	4552	G	G	G	G	A	A	G	G	G
4359-5177	PS16	4822	C	C	C	C	C	C	C	C	C
4359-5177	PS17	4999	T	C	T	T	T	T	T	C	T
4359-5177	PS18	5077	T	T	T	T	C	C	T	T	T
6200-7073	PS19	6535	C	C	C	C	C	C	C	C	C
6200-7073	PS20	6625	T	T	T	T	T	T	T	T	T
6200-7073	PS21	6650	A	A	A	A	A	G	A	A	A
6200-7073	PS22	6714	G	A	G	G	G	G	G	G	G

Regions Examined(a)	PS Number(b)	PS Position (c)	Isogene Number(d) (Part 2)									
			11	12	13	14	15	16	17	18	19	20
319-1709	PS1	586	G	T	T	T	T	T	T	T	T	T
319-1709	PS2	657	C	C	C	T	C	C	C	C	T	T
319-1709	PS3	906	T	T	T	T	T	T	T	T	T	T
319-1709	PS4	913	A	A	A	A	A	A	A	T	A	A
319-1709	PS5	1077	C	C	C	C	C	C	C	C	C	A
319-1709	PS6	1468	C	T	T	T	T	T	T	T	T	T
319-1709	PS7	1474	C	C	C	C	A	C	C	C	C	C
319-1709	PS8	1610	C	C	T	T	T	C	T	T	C	T
2351-3067	PS9	2422	A	A	A	A	A	A	A	A	A	A
2351-3067	PS10	2738	A	A	A	A	A	A	G	A	A	A
2351-3067	PS11	2789	G	G	G	G	G	G	G	G	G	G
2351-3067	PS12	2934	C	T	T	T	T	T	T	T	T	T
2351-3067	PS13	3000	G	G	G	G	G	G	G	G	G	G
2351-3067	PS14	3044	G	G	G	G	G	A	G	G	G	G
4359-5177	PS15	4552	G	G	A	G	G	G	G	A	G	A
4359-5177	PS16	4822	C	C	C	C	C	C	C	C	T	C
4359-5177	PS17	4999	T	T	T	C	T	T	T	T	C	C
4359-5177	PS18	5077	T	T	C	T	T	T	T	C	T	C
6200-7073	PS19	6535	C	A	C	C	C	A	C	C	C	C
6200-7073	PS20	6625	C	T	T	T	T	T	T	T	T	T
6200-7073	PS21	6650	A	A	G	A	A	A	A	A	A	A
6200-7073	PS22	6714	G	G	G	A	G	G	G	G	A	G

(a) Region examined represents the nucleotide positions defining the start and stop positions within SEQ ID NO:1 of the regions sequenced;
(b) PS = polymorphic site;
(c) Position of PS within SEQ ID NO:1;
(d) Alleles for FCER1A isogenes are presented 5′ to 3′ in each column.

23. An isolated polynucleotide comprising a coding sequence for a FCER1A isogene, wherein the coding sequence comprises the regions of SEQ ID NO:2, except at each of the polymorphic sites which have the positions in SEQ ID NO:2 and polymorphisms set forth in the table immediately below:

Regions Examined(a)	PS Number(b)	Position (c)	Isogene Coding Sequence Number(d)					
			7	10	12	16	17	19
1-774	**PS10**	251	G	A	A	A	G	A
1-774	**PS11**	302	G	A	G	G	G	G
1-774	**PS16**	503	C	C	C	C	C	T
1-774	**PS19**	741	C	C	A	A	C	C

(a) Region examined represents the nucleotide positions defining the start and stop positions within SEQ ID NO:2 of the regions sequenced;
(b) PS = polymorphic site;
(c) Position of PS within SEQ ID NO:2;
(d) Alleles for FCER1A isogenes are presented 5′ to 3′ in each column.

24. A recombinant nonhuman organism transformed or transfected with the isolated polynucleotide of claim 23, wherein the organism expresses a Fc fragment of IgE, high affinity I, receptor for; alpha polypeptide (FCER1A) protein that is encoded by the polymorphic variant sequence.

25. The recombinant nonhuman organism of claim 24, which is a transgenic animal.

26. An isolated fragment of a FCER1A coding sequence, wherein the fragment comprises one or more polymorphisms selected from the group consisting of guanine at a position corresponding to nucleotide 251, adenine at a position corresponding to nucleotide 302, thymine at a position corresponding to nucleotide 530 and adenine at a position corresponding to nucleotide 741 in SEQ ID NO:2.

27. An isolated polypeptide comprising an amino acid sequence which is a polymorphic variant of a reference sequence for the Fc fragment of IgE, high affinity I, receptor for; alpha polypeptide (FCER1A) protein, wherein the reference sequence comprises SEQ ID NO:3, except the polymorphic variant comprises one or more variant amino acids selected from the group consisting of arginine at a position corresponding to amino acid position 84, asparagine at a position corresponding to amino acid position 101, methionine at a position corresponding to amino acid position 177 and lysine at a position corresponding to amino acid position 247.

28. An isolated monoclonal antibody specific for and immunoreactive with the isolated polypeptide of claim 27.

29. A method for screening for drugs targeting the isolated polypeptide of claim 27 which comprises contacting the FCER1A polymorphic variant with a candidate agent and assaying for binding activity.

30. An isolated fragment of a FCER1A protein, wherein the fragment comprises one or more variant amino acids selected from the group consisting of arginine at a position corresponding to amino acid position 84, asparagine at a position corresponding to amino acid position 101, methionine at a position corresponding to amino acid position 177 and lysine at a position corresponding to amino acid position 247 in SEQ ID NO:3.

31. A computer system for storing and analyzing polymorphism data for the Fc fragment of IgE, high affinity I, receptor for; alpha polypeptide gene, comprising:

(a) a central processing unit (CPU);

(b) a communication interface;

(c) a display device;

(d) an input device; and

(e) a database containing the polymorphism data;

wherein the polymorphism data comprises any one or more of the haplotypes set forth in the table immediately below:

PS Number(a)	PS Position (b)	Haplotype Number(c)									
		1	2	3	4	5	6	7	8	9	10
PS1	586	T	T	T	T	G	T	T	T	T	T
PS2	657	C	T	T	C	C	C	C	C	T	C
PS3	906	T	T	T	C	T	T	T	T	T	T
PS4	913	A	A	A	A	A	A	A	A	A	A
PS5	1077	C	C	C	C	C	C	C	C	C	C
PS6	1468	T	T	T	T	T	T	T	T	T	T
PS7	1474	C	C	C	C	C	C	C	C	C	C
PS8	1610	C	C	C	C	C	T	T	T	C	T
PS9	2422	A	A	A	A	A	A	A	A	G	A
PS10	2738	A	A	A	A	A	A	G	A	A	A
PS11	2789	G	G	G	G	G	G	G	G	G	A
PS12	2934	T	T	T	T	T	T	T	T	T	T
PS13	3000	G	G	G	G	G	G	G	G	G	A
PS14	3044	G	G	G	G	G	G	G	G	G	G
PS15	4552	G	G	G	G	G	A	A	G	G	G
PS16	4822	C	C	C	C	C	C	C	C	C	C
PS17	4999	T	C	C	T	T	T	T	T	C	T
PS18	5077	T	T	T	T	T	C	C	T	T	T
PS19	6535	C	C	C	C	C	C	C	C	C	C
PS20	6625	T	T	T	T	T	T	T	T	T	T
PS21	6650	A	A	A	A	A	A	G	A	A	A
PS22	6714	G	G	A	G	G	G	G	G	G	G

PS Number(a)	PS Position (b)	Haplotype Number(c)									
		11	12	13	14	15	16	17	18	19	20
PS1	586	G	T	T	T	T	T	T	T	T	T
PS2	657	C	C	C	T	C	C	C	C	T	T
PS3	906	T	T	T	T	T	T	T	T	T	T
PS4	913	A	A	A	A	A	A	A	T	A	A
PS5	1077	C	C	C	C	C	C	C	C	C	A
PS6	1468	C	T	T	T	T	T	T	T	T	T
PS7	1474	C	C	C	C	A	C	C	C	C	C
PS8	1610	C	C	T	T	T	C	T	T	C	T
PS9	2422	A	A	A	A	A	A	A	A	A	A
PS10	2738	A	A	A	A	A	A	G	A	A	A
PS11	2789	G	G	G	G	G	G	G	G	G	G
PS12	2934	C	T	T	T	T	T	T	T	T	T
PS13	3000	G	G	G	G	G	G	G	G	G	G
PS14	3044	G	G	G	G	G	A	G	G	G	G
PS15	4552	G	G	A	G	G	G	G	A	G	A
PS16	4822	C	C	C	C	C	C	C	C	T	C
PS17	4999	T	T	T	C	T	T	T	T	C	C
PS18	5077	T	T	C	T	T	T	T	C	T	C
PS19	6535	C	A	C	C	C	A	C	C	C	C
PS20	6625	C	T	T	T	T	T	T	T	T	T
PS21	6650	A	A	G	A	A	A	A	A	A	A
PS22	6714	G	G	G	A	G	G	G	G	A	G

(a) PS = polymorphic site;
(b) Position of PS within SEQ ID NO:1;
(c) Alleles for haplotypes are presented 5′ to 3′ in each column;

the haplotype pairs set forth in the table immediately below:

PS Number(a)	PS Position(b)	Haplotype Pair(c) Part 1														
		1/1	1/2	1/3	1/4	1/5	1/7	1/11	1/12	1/15	1/16	1/17	1/20	2/2	2/3	2/4
PS1	586	T	T	T	T	T/G	T	T/G	T	T	T	T	T	T	T	T
PS2	657	C	C/T	C/T	C	C	C	C	C	C	C	C	C/T	T	T	C/T
PS3	906	T	T	T	T/C	T	T	T	T	T	T	T	T	T	T	T/C
PS4	913	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A
PS5	1077	C	C	C	C	C	C	C	C	C	C	C	C/A	C	C	C
PS6	1468	T	T	T	T	T	T	T/C	T	T	T	T	T	T	T	T
PS7	1474	C	C	C	C	C	C	C	C	C/A	C	C	C	C	C	C
PS8	1610	C	C	C	C	C	C/T	C	C	C/T	C	C/T	C/T	C	C	C
PS9	2422	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A
PS10	2738	A	A	A	A	A	A/G	A	A	A	A	A/G	A	A	A	A
PS11	2789	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G
PS12	2934	T	T	T	T	T	T	T/C	T	T	T	T	T	T	T	T
PS13	3000	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G
PS14	3044	G	G	G	G	G	G	G	G	G	G/A	G	G	G	G	G
PS15	4552	G	G	G	G	G	G/A	G	G	G	G	G	G/A	G	G	G
PS16	4822	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C
PS17	4999	T	T/C	T/C	T	T	T	T	T	T	T	T	T/C	C	C	T/C
PS18	5077	T	T	T	T	T	T/C	T	T	T	T	T/C	T/C	T	T	T
PS19	6535	C	C	C	C	C	C	C	C/A	C	C/A	C	C	C	C	C
PS20	6625	T	T	T	T	T	T	T/C	T	T	T	T	T	T	T	T
PS21	6650	A	A	A	A	A	A/G	A	A	A	A	A	A	A	A	A
PS22	6714	G	G	G/A	G	G	G	G	G	G	G	G	G	G	G/A	G

PS Number(a)	PS Position(b)	Haplotype Pair(c) Part 2														
		2/6	2/9	2/10	2/13	2/14	3/3	3/4	3/5	3/6	3/9	3/12	3/15	3/19	4/4	4/5
PS1	586	T	T	T	T	T	T	T	T/G	T	T	T	T	T	T	T/G
PS2	657	C/T	T	C/T	C/T	T	T	C/T	C/T	C/T	T	C/T	C/T	T	C	C
PS3	906	T	T	T	T	T	T	T/C	T	T	T	T	T	T	C	T/C
PS4	913	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A
PS5	1077	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C
PS6	1468	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T
PS7	1474	C	C	C	C	C	C	C	C	C	C	C	C/A	C	C	C
PS8	1610	C/T	C	C/T	C/T	C/T	C	C	C	C/T	C	C	C/T	C	C	C
PS9	2422	A	A/G	A	A	A	A	A	A	A	A/G	A	A	A	A	A
PS10	2738	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A
PS11	2789	G	G	G/A	G	G	G	G	G	G	G	G	G	G	G	G
PS12	2934	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T
PS13	3000	G	G	G/A	G	G	G	G	G	G	G	G	G	G	G	G
PS14	3044	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G
PS15	4552	G/A	G	G	G/A	G	G	G	G	G/A	G	G	G	G	G	G
PS16	4822	C	C	C	C	C	C	C	C	C	C	C	C	C/T	C	C
PS17	4999	T/C	C	T/C	T/C	T/C	C	T/C	T/C	T/C	C	T/C	T/C	C	T	T
PS18	5077	T/C	T	T	T/C	T	T	T	T	T/C	T	T	T	T	T	T
PS19	6535	C	C	C	C	C	C	C	C	C	C	C/A	C	C	C	C
PS20	6625	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T
PS21	6650	A	A	A	A/G	A	A	A	A	A	A	A	A	A	A	A
PS22	6714	G	G	G	G	G/A	A	G/A	G/A	G/A	G/A	G/A	G/A	A	G	G

PS Number(a)	PS Position(b)	Haplotype Pair(c) Part 3													
		4/6	4/8	4/11	4/13	5/5	5/11	5/15	6/6	6/7	6/8	6/10	6/18	7/7	7/10
PS1	586	T	T	T/G	T	G	G	T/G	T	T	T	T	T	T	T
PS2	657	C	C	C	C	C	C	C	C	C	C	C	C	C	C
PS3	906	T/C	T/C	T/C	T/C	T	T	T	T	T	T	T	T	T	T
PS4	913	A	A	A	A	A	A	A	A	A	A	A	A/T	A	A
PS5	1077	C	C	C	C	C	C	C	C	C	C	C	C	C	C
PS6	1468	T	T	T/C	T	T	T/C	T	T	T	T	T	T	T	T
PS7	1474	C	C	C	C	C	C	C/A	C	C	C	C	C	C	C
PS8	1610	C/T	C/T	C	C/T	C	C	C/T	T	T	T	T	T	T	T
PS9	2422	A	A	A	A	A	A	A	A	A	A	A	A	A	A
PS10	2738	A	A	A	A	A	A	A	A	A/G	A	A	A	G	A/G
PS11	2789	G	G	G	G	G	G	G	G	G	G	G/A	G	G	G/A
PS12	2934	T	T	T/C	T	T	T/C	T	T	T	T	T	T	T	T
PS13	3000	G	G	G	G	G	G	G	G	G	G	G/A	G	G	G/A
PS14	3044	G	G	G	G	G	G	G	G	G	G	G	G	G	G
PS15	4552	G/A	G	G	G/A	G	G	G	A	A	G/A	G/A	A	A	G/A
PS16	4822	C	C	C	C	C	C	C	C	C	C	C	C	C	C
PS17	4999	T	T	T	T	T	T	T	T	T	T	T	T	T	T
PS18	5077	T/C	T	T	T/C	T	T	T	C	C	T/C	T/C	C	C	T/C
PS19	6535	C	C	C	C	C	C	C	C	C	C	C	C	C	C
PS20	6625	T	T	T/C	T	T	T/C	T	T	T	T	T	T	T	T
PS21	6650	A	A	A	A/G	A	A	A	A	A/G	A	A	A	G	A/G
PS22	6714	G	G	G	G	G	G	G	G	G	G	G	G	G	G

(a) PS = polymorphic site;
(b) Position of PS in SEQ ID NO:1;
(c) Haplotype pairs are represented as 1st haplotype/2nd haplotype; with alleles of each haplotype shown 5′ to 3′ as 1st polymorphism/2nd polymorphism in each column;

and the frequency data in Tables 6 and 7.

32. A genome anthology for the Fc fragment of IgE, high affinity I, receptor for; alpha polypeptide (FCER1A) gene which comprises two or more FCER1A isogenes selected from the group consisting of isogenes 1-20 shown in the table immediately below, and wherein each of the isogenes comprises the regions of SEQ ID NO:1 shown in the table immediately below and wherein each of the isogenes 1-20 is further defined by the corresponding sequence of polymorphisms whose positions and identities are set forth in the table immediately below:

Regions Examined(a)	PS Number(b)	PS Position(c)	Isogene Number(d) (Part 1)									
			1	2	3	4	5	6	7	8	9	10
319-1709	PS1	586	T	T	T	T	G	T	T	T	T	T
319-1709	PS2	657	C	T	T	C	C	C	C	C	T	C
319-1709	PS3	906	T	T	T	C	T	T	T	T	T	T
319-1709	PS4	913	A	A	A	A	A	A	A	A	A	A
319-1709	PS5	1077	C	C	C	C	C	C	C	C	C	C
319-1709	PS6	1468	T	T	T	T	T	T	T	T	T	T
319-1709	PS7	1474	C	C	C	C	C	C	C	C	C	C
319-1709	PS8	1610	C	C	C	C	C	T	T	T	C	T
2351-3067	PS9	2422	A	A	A	A	A	A	A	A	G	A
2351-3067	PS10	2738	A	A	A	A	A	A	G	A	A	A
2351-3067	PS11	2789	G	G	G	G	G	G	G	G	G	A
2351-3067	PS12	2934	T	T	T	T	T	T	T	T	T	T
2351-3067	PS13	3000	G	G	G	G	G	G	G	G	G	A
2351-3067	PS14	3044	G	G	G	G	G	G	G	G	G	G
4359-5177	PS15	4552	G	G	G	G	G	A	A	G	G	G
4359-5177	PS16	4822	C	C	C	C	C	C	C	C	C	C
4359-5177	PS17	4999	T	C	C	T	T	T	T	T	C	T
4359-5177	PS18	5077	T	T	T	T	T	C	C	T	T	T
6200-7073	PS19	6535	C	C	C	C	C	C	C	C	C	C
6200-7073	PS20	6625	T	T	T	T	T	T	T	T	T	T
6200-7073	PS21	6650	A	A	A	A	A	A	G	A	A	A
6200-7073	PS22	6714	G	G	A	G	G	G	G	G	G	G

Regions Examined(a)	PS Number(b)	PS Position(c)	Isogene Number(d) (Part 2)									
			11	12	13	14	15	16	17	18	19	20
319-1709	PS1	586	G	T	T	T	T	T	T	T	T	T
319-1709	PS2	657	C	C	C	T	C	C	C	C	T	T
319-1709	PS3	906	T	T	T	T	T	T	T	T	T	T
319-1709	PS4	913	A	A	A	A	A	A	A	T	A	A
319-1709	PS5	1077	C	C	C	C	C	C	C	C	C	A
319-1709	PS6	1468	C	T	T	T	T	T	T	T	T	T
319-1709	PS7	1474	C	C	C	C	A	C	C	C	C	C
319-1709	PS8	1610	C	C	T	T	T	C	T	T	C	T
2351-3067	PS9	2422	A	A	A	A	A	A	A	A	A	A
2351-3067	PS10	2738	A	A	A	A	A	A	G	A	A	A
2351-3067	PS11	2789	G	G	G	G	G	G	G	G	G	G
2351-3067	PS12	2934	C	T	T	T	T	T	T	T	T	T
2351-3067	PS13	3000	G	G	G	G	G	G	G	G	G	G
2351-3067	PS14	3044	G	G	G	G	G	A	G	G	G	G
4359-5177	PS15	4552	G	G	A	G	G	G	G	A	G	A
4359-5177	PS16	4822	C	C	C	C	C	C	C	C	T	C
4359-5177	PS17	4999	T	T	T	C	T	T	T	T	C	C
4359-5177	PS18	5077	T	T	C	T	T	T	T	C	T	C
6200-7073	PS19	6535	C	A	C	C	C	A	C	C	C	C
6200-7073	PS20	6625	C	T	T	T	T	T	T	T	T	T
6200-7073	PS21	6650	A	A	G	A	A	A	A	A	A	A
6200-7073	PS22	6714	G	G	G	A	G	G	G	G	A	G

(a) Region examined represents the nucleotide positions defining the start and stop positions within SEQ ID NO:1 of the regions sequenced;
(b) PS = polymorphic site;
(c) IPosition of PS within SEQ ID NO:1;
(d) Alleles for FCER1A isogenes are presented 5′ to 3′ in each column.